

## Supplementary Information

**Autophagy maintains the metabolism and function of young and old (hematopoietic) stem cells.** Ho, T.T., Warr, M.R., Adelman, E., Lansinger, O.M., Flach, J., Verovskaya, E.V., Figueroa, M.E. & Passegué, E.

**Supplementary Table 1 | Functional annotation of autophagy-deficient HSC and GMP microarray gene expression analyses.**

<b>HSCs</b>				
Term	Count	Fold Enrichment	Benjamini	FDR
<i>Downregulated DEGs</i>				
Negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	5	43.4	2.6E-03	7.0E-03
Antigen processing and presentation	6	15.7	2.7E-03	3.3E-02
Immune response	8	8.2	1.2E-02	6.3E-02
<i>Upregulated DEGs</i>				
Response to virus	8	38.8	3.3E-07	1.5E-06
Defense response to virus	8	19.6	1.9E-05	1.7E-04
Double-stranded RNA binding	6	36.6	4.8E-05	5.7E-04
<b>GMPs</b>				
Term	Count	Fold Enrichment	Benjamini	FDR
<i>Downregulated DEGs</i>				
Acetylation	70	2.80	4.1E-13	4.6E-18
Phosphoprotein	67	2.77	1.2E-12	5.9E-13
Nucleus	67	2.78	1.6E-12	8.0E-12
Nucleus	107	2.09	1.6E-11	6.3E-11
Cytoplasm	29	4.40	5.8E-09	5.3E-06
Mitochondrion	63	2.24	5.3E-08	7.5E-06
Mitochondrion	48	2.56	1.5E-07	7.1E-05
rRNA processing	132	1.57	2.2E-06	2.3E-04
Nucleolus	17	6.78	5.6E-06	2.5E-04
Cytoplasm	18	5.87	8.0E-06	3.1E-04
Ribosome biogenesis	72	1.76	3.4E-05	8.2E-04
Ribosome biogenesis	72	1.76	3.4E-05	4.3E-03
Nucleoplasm	28	2.85	5.8E-05	6.2E-03

Poly(A) RNA binding	30	2.69	6.3E-05	9.5E-03
Redox-active center	41	2.36	8.3E-05	5.9E-02
rRNA processing	19	4.20	3.3E-04	8.1E-02
Hydrolase	28	2.43	7.8E-04	8.3E-02

*Upregulated DEGs*

Immunity	33	4.3	3.3E-09	1.6E-08
Immune system process	32	4.3	3.2E-08	3.2E-08
Response to virus	16	9.6	7.1E-08	1.4E-07
Innate immunity	24	5.3	3.1E-08	3.1E-07
Defense response to virus	19	5.8	2.8E-06	8.6E-06
Antiviral defense	15	7.8	6.7E-07	1.0E-05
Innate immune response	26	3.3	1.5E-04	6.1E-04
Staphylococcus aureus infection	8	7.5	1.6E-02	9.9E-02

DAVID analyses of downregulated and upregulated (FDR < 0.1) differentially expressed genes (DEG) with a p-value < 0.01 between Cnt and *Atg12<sup>CKO</sup>* HSCS or GMPs (n = 4).

**Supplementary Table 2 | Fluidigm qRT-PCR measurements of gene expression changes in autophagy-deficient and activated HSCs.**

<i>Genes</i>	<i>Atg12<sup>CKO</sup></i> HSC	aHSC
<i>Axin2</i>	1.72 ± 0.13*	0.43 ± 0.10
<i>Bax</i>	1.35 ± 0.37	2.78 ± 0.48*
<i>Bbc3</i>	n.d.	0.30 ± 0.13*
<i>Bcl2</i>	1.10 ± 0.20	0.58 ± 0.03
<i>Bcl2l1</i>	1.13 ± 0.21	1.46 ± 0.19***
<i>Birc2</i>	0.91 ± 0.07	0.39 ± 0.04***
<i>Bmi1</i>	0.92 ± 0.13	0.63 ± 0.07**
<i>Cbx7</i>	0.89 ± 0.20	0.27 ± 0.05***
<i>Ccl3</i>	0.73 ± 0.54	0.09 ± 0.04**
<i>Ccna2</i>	1.42 ± 0.37	1.64 ± 0.22
<i>Ccnb1</i>	1.04 ± 0.21	0.43 ± 0.09***
<i>Ccnd1</i>	1.49 ± 0.17	0.92 ± 0.18
<i>Ccne1</i>	1.24 ± 0.89	2.04 ± 0.35
<i>Cd34</i>	1.28 ± 0.45	0.59 ± 0.06*
<i>Cd48</i>	1.45 ± 0.64	3.59 ± 0.87*
<i>Cdc20</i>	1.04 ± 0.23	0.35 ± 0.1**
<i>Cdk2</i>	0.26 ± 0.09	3.47 ± 0.49
<i>Cdkn1b</i>	0.89 ± 0.18	0.36 ± 0.06**
<i>Cebpa</i>	0.85 ± 0.23	0.93 ± 0.52
<i>Csf1r</i>	0.56 ± 0.28	0.28 ± 0.13*
<i>Csf2ra</i>	0.89 ± 0.30	0.29 ± 0.08**
<i>Csf3r</i>	0.76 ± 0.04**	0.74 ± 0.24
<i>Dnmt3a</i>	0.87 ± 0.10	0.45 ± 0.05**
<i>Egr1</i>	0.65 ± 0.21	0.10 ± 0.01**
<i>Epor</i>	0.91 ± 0.06	1.05 ± 0.19
<i>Ezh1</i>	0.79 ± 0.06*	0.32 ± 0.06**
<i>Ezh2</i>	1.33 ± 0.20	0.94 ± 0.11
<i>Flt3</i>	1.44 ± 0.48	0.36 ± 0.05**
<i>Fnl1</i>	1.62 ± 1.85	4.28 ± 0.77*
<i>Foxo3</i>	0.72 ± 0.11	0.42 ± 0.06**
<i>Fzd2</i>	6.97 ± 5.02	0.13 ± 0.05*
<i>Gata2</i>	0.98 ± 0.22	0.50 ± 0.02***
<i>Gfi1</i>	0.66 ± 0.08	0.29 ± 0.16*
<i>Gfi1b</i>	1.10 ± 0.45	0.63 ± 0.11
<i>Hes1</i>	1.57 ± 0.55	0.05 ± 0.04*
<i>Hes5</i>	1.27 ± 0.28	0.79 ± 0.06
<i>Hhip</i>	n.d.	n.d.
<i>Hif1a</i>	0.85 ± 0.15	1.08 ± 0.12
<i>Id1</i>	0.47 ± 0.21	1.73 ± 0.37
<i>Ikzf1</i>	0.98 ± 0.18	0.75 ± 0.07
<i>Il6</i>	0.55 ± 0.29	0.09 ± 0.03***
<i>Il7r</i>	0.60 ± 0.26	0.12 ± 0.13**

<i>Irf8</i>	0.68 ± 0.17	0.35 ± 0.17*
<i>Jun</i>	1.00 ± 0.08	0.02 ± 0.00***
<i>Lrp5</i>	0.80 ± 0.10	0.95 ± 0.10
<i>Mcl1</i>	0.89 ± 0.22	1.02 ± 0.11
<i>Mfng</i>	0.84 ± 0.04*	0.44 ± 0.05***
<i>Mki67</i>	1.58 ± 0.31	1.49 ± 0.18
<i>Mpl</i>	0.74 ± 0.12	0.40 ± 0.05***
<i>Myc</i>	1.14 ± 0.32	0.65 ± 0.08*
<i>Nfe2l2</i>	0.74 ± 0.04**	0.63 ± 0.10*
<i>Nfkbia</i>	0.87 ± 0.07	0.32 ± 0.06**
<i>Pax5</i>	1.03 ± 0.43	0.11 ± 0.03*
<i>Pdk4</i>	0.71 ± 0.19	0.09 ± 0.05**
<i>Prkdc</i>	1.15 ± 0.01	0.58 ± 0.06*
<i>Ptch1</i>	0.82 ± 0.05*	0.72 ± 0.06**
<i>Rad51</i>	1.30 ± 0.26	2.06 ± 0.41
<i>Rpa1</i>	1.16 ± 0.22	1.56 ± 0.10*
<i>Runx1</i>	0.96 ± 0.25	0.84 ± 0.07
<i>Sfp1</i>	0.92 ± 0.11	0.90 ± 0.15
<i>Slamf1</i>	0.95 ± 0.22	0.80 ± 0.14
<i>Smad7</i>	0.71 ± 0.07	0.39 ± 0.13*
<i>Xiap</i>	0.94 ± 0.09	0.53 ± 0.06**
<i>Xrcc5</i>	0.98 ± 0.10	0.75 ± 0.09
<i>Xrcc6</i>	0.97 ± 0.09	0.77 ± 0.06
<i>Zfpml</i>	1.05 ± 0.39	0.29 ± 0.02**

HSCs isolated from either control (Cnt) or *Atg12<sup>KO</sup>* mice (n = 3), and freshly isolated wild type quiescent HSCs (qHSC) or HSCs activated (aHSC) by 21hr +cyt *in vitro* culture (n = 4) were used for Fluidigm gene expression analyses (3 technical pools of 100 cells/mouse). Results are mean ± SD and are expressed as fold changes compared to levels in Cnt HSCs for *Atg12<sup>KO</sup>* HSCs, and qHSCs for aHSCs; n.d., not detected, \*p ≤ 0.05; \*\*p ≤ 0.01, \*\*\*p ≤ 0.001.

**Supplementary Table 3 | Fluidigm qRT-PCR measurements of gene expression changes in autophagy-deficient MPPs.**

<i>Genes</i>	<b>MPP2</b>		<b>MPP3</b>		<b>MPP4</b>	
	<b>Cnt</b>	<i>Atg12<sup>CKO</sup></i>	<b>Cnt</b>	<i>Atg12<sup>CKO</sup></i>	<b>Cnt</b>	<i>Atg12<sup>CKO</sup></i>
<i>Axin2</i>	2.69 ± 0.99	3.09 ± 0.83	1.41 ± 0.32	1.27 ± 0.84	1.00 ± 0.62	0.76 ± 0.25
<i>Bax</i>	0.76 ± 0.14	0.84 ± 0.16	1.23 ± 0.11	1.06 ± 0.20	0.61 ± 0.04	0.71 ± 0.11
<i>Bbc3</i>	0.23 ± 0.21	0.55 ± 0.23	n.d.	n.d.	0.54 ± 0.39	n.d.
<i>Bcl2</i>	0.85 ± 0.12	0.96 ± 0.13**	0.58 ± 0.05	0.82 ± 0.14*	1.22 ± 0.06	1.46 ± 0.32
<i>Bcl2l1</i>	0.50 ± 0.10	0.71 ± 0.12	0.97 ± 0.20	0.71 ± 0.06	0.44 ± 0.11	0.45 ± 0.02
<i>Birc2</i>	0.47 ± 0.09	0.49 ± 0.09	0.40 ± 0.14	0.40 ± 0.06	0.62 ± 0.22	0.48 ± 0.02
<i>Bmi1</i>	0.46 ± 0.06	0.59 ± 0.07*	0.46 ± 0.06	0.48 ± 0.05	0.50 ± 0.06	0.48 ± 0.00
<i>Cbx7</i>	0.34 ± 0.05	0.41 ± 0.06	0.11 ± 0.04	0.13 ± 0.05	0.55 ± 0.24	0.37 ± 0.03
<i>Ccl3</i>	0.95 ± 0.23	0.94 ± 0.27	1.52 ± 0.51	1.55 ± 0.66	5.23 ± 2.21	5.27 ± 2.05
<i>Ccna2</i>	1.50 ± 0.56	2.24 ± 0.28	1.69 ± 0.13	1.49 ± 0.13	1.24 ± 0.29	1.40 ± 0.08
<i>Ccnbl</i>	1.76 ± 0.22	1.75 ± 0.11	2.18 ± 0.34	2.09 ± 0.26	2.40 ± 0.31	2.79 ± 0.31
<i>Ccnd1</i>	0.26 ± 0.03	0.41 ± 0.09*	0.12 ± 0.05	0.25 ± 0.17	0.82 ± 0.21	0.84 ± 0.32
<i>Ccne1</i>	1.63 ± 0.39	1.89 ± 0.08	1.44 ± 0.16	1.29 ± 0.10	1.01 ± 0.17	1.00 ± 0.05
<i>Cd34</i>	0.75 ± 0.29	1.23 ± 0.19	1.35 ± 0.33	1.57 ± 0.68	2.72 ± 0.19	2.88 ± 0.23
<i>Cd48</i>	23.3 ± 6.88	32.4 ± 9.99*	47.9 ± 10.1	46.5 ± 5.24	30.7 ± 11.3	46.3 ± 1.74
<i>Cdc20</i>	1.66 ± 0.33	1.7 ± 0.27	1.73 ± 0.24	2.13 ± 0.36	2.93 ± 0.55	3.38 ± 0.50
<i>Cdk2</i>	0.44 ± 0.37	0.16 ± 0.10*	0.40 ± 0.25	0.12 ± 0.08**	0.22 ± 0.12	0.17 ± 0.04
<i>Cdkn1b</i>	0.59 ± 0.12	0.74 ± 0.15	0.37 ± 0.07	0.46 ± 0.1**	0.57 ± 0.07	0.55 ± 0.04
<i>Cebpa</i>	8.74 ± 3.31	8.93 ± 3.4	34.2 ± 4.13	32.9 ± 0.18	15.8 ± 0.73	15.7 ± 3.42
<i>Csf1r</i>	2.49 ± 0.94	1.69 ± 0.53	4.14 ± 0.54	3.75 ± 0.51	4.33 ± 1.02	5.21 ± 1.25
<i>Csf2ra</i>	0.53 ± 0.21	0.67 ± 0.13	0.57 ± 0.17	0.69 ± 0.15	0.49 ± 0.07	0.48 ± 0.05
<i>Csf3r</i>	0.40 ± 0.01	0.49 ± 0.07	1.45 ± 0.46	1.35 ± 0.24	1.39 ± 0.33	1.22 ± 0.13
<i>Dnmt3a</i>	0.39 ± 0.08	0.56 ± 0.16	0.43 ± 0.10	0.49 ± 0.05	0.76 ± 0.07	0.67 ± 0.08
<i>Egr1</i>	0.42 ± 0.44	0.55 ± 0.39	0.05 ± 0.03	0.09 ± 0.06	0.19 ± 0.17	0.15 ± 0.12
<i>Epor</i>	2.01 ± 1.08	1.80 ± 0.45	0.14 ± 0.11	0.10 ± 0.07	n.d.	n.d.
<i>Ezh1</i>	0.27 ± 0.08	0.34 ± 0.02	0.33 ± 0.07	0.34 ± 0.07	0.55 ± 0.17	0.52 ± 0.08
<i>Ezh2</i>	1.65 ± 0.33	1.64 ± 0.08	1.44 ± 0.3	1.26 ± 0.06	1.32 ± 0.36	1.18 ± 0.07
<i>Flt3</i>	0.43 ± 0.21	1.00 ± 0.38	0.81 ± 0.42	1.32 ± 0.71	15.9 ± 3.27	17.0 ± 3.87
<i>Fnl</i>	0.81 ± 0.91	1.07 ± 0.72	0.22 ± 0.06	0.21 ± 0.13	0.18 ± 0.11	0.29 ± 0.21
<i>Foxo3</i>	0.42 ± 0.22	0.63 ± 0.07	0.23 ± 0.02	0.30 ± 0.12	0.57 ± 0.21	0.52 ± 0.02
<i>Fzd2</i>	12.2 ± 4.94	9.16 ± 8.06	7.86 ± 2.89	11.8 ± 1.04	49.9 ± 23.7	33.6 ± 3.27
<i>Gata2</i>	0.68 ± 0.22	0.96 ± 0.29	0.14 ± 0.02	0.21 ± 0.11	0.11 ± 0.03	0.11 ± 0.00
<i>Gfi1</i>	0.93 ± 0.21	0.56 ± 0.46	6.39 ± 0.68	5.98 ± 0.88	2.48 ± 0.40	2.67 ± 0.38
<i>Gfi1b</i>	0.82 ± 0.26	1.09 ± 0.32	0.16 ± 0.08	0.21 ± 0.08	0.19 ± 0.06	0.15 ± 0.02
<i>Hes1</i>	0.39 ± 0.36	0.49 ± 0.2	n.d.	0.62 ± 0.64	0.17 ± 0.17	n.d.
<i>Hes5</i>	0.70 ± 0.27	0.56 ± 0.28	0.36 ± 0.16	0.44 ± 0.07	2.85 ± 1.19	1.96 ± 0.61
<i>Hhip</i>	0.79 ± 0.20	0.54 ± 0.31	1.56 ± 0.78	1.22 ± 0.64	1.39 ± 0.36	2.77 ± 0.46

<i>Hif1a</i>	0.67 ± 0.09	0.57 ± 0.04	1.16 ± 0.41	0.96 ± 0.17	0.64 ± 0.16	0.61 ± 0.06
<i>Id1</i>	1.28 ± 0.52	1.43 ± 0.51	1.22 ± 0.46	1.90 ± 0.49*	3.46 ± 2.04	2.86 ± 0.67
<i>Ikzf1</i>	0.98 ± 0.40	1.06 ± 0.16	1.20 ± 0.07	1.10 ± 0.07	1.25 ± 0.13	1.23 ± 0.08
<i>Il6</i>	1.44 ± 0.36	1.33 ± 0.39	1.48 ± 0.32	1.73 ± 0.32	4.03 ± 2.10	3.18 ± 0.54
<i>Il7r</i>	1.98 ± 0.41	1.44 ± 0.24	1.93 ± 0.53	2.30 ± 0.21	4.16 ± 0.92	4.69 ± 1.16
<i>Irf8</i>	7.35 ± 3.42	4.23 ± 4.33	8.99 ± 5.57	11.2 ± 0.87	6.65 ± 3.11	9.99 ± 2.98
<i>Jun</i>	0.97 ± 0.52	1.39 ± 0.53	0.36 ± 0.13	0.44 ± 0.10	0.53 ± 0.18	0.55 ± 0.11
<i>Lrp5</i>	0.43 ± 0.09	0.53 ± 0.08	0.52 ± 0.06	0.50 ± 0.04	1.07 ± 0.26	1.11 ± 0.13
<i>Mcl1</i>	0.36 ± 0.10	0.49 ± 0.12	0.50 ± 0.05	0.52 ± 0.08	0.35 ± 0.01	0.35 ± 0.05
<i>Mfng</i>	0.25 ± 0.04	0.30 ± 0.04	0.25 ± 0.04	0.27 ± 0.03	0.57 ± 0.18	0.49 ± 0.06
<i>Mki67</i>	2.26 ± 0.11	2.38 ± 0.30	1.67 ± 0.44	1.43 ± 0.33	1.26 ± 0.05	1.17 ± 0.18
<i>Mpl</i>	0.17 ± 0.04	0.23 ± 0.04	0.11 ± 0.00	0.14 ± 0.02	0.28 ± 0.10	0.25 ± 0.04
<i>Myc</i>	1.13 ± 0.07	1.16 ± 0.24	1.52 ± 0.59	1.35 ± 0.37	1.46 ± 0.30	1.54 ± 0.46
<i>Nfe2l2</i>	0.60 ± 0.08	0.60 ± 0.03	0.67 ± 0.06	0.63 ± 0.03	0.79 ± 0.21	0.71 ± 0.14
<i>Nfkbia</i>	0.58 ± 0.14	0.57 ± 0.07	0.78 ± 0.27	0.62 ± 0.04	0.68 ± 0.20	0.66 ± 0.06
<i>Pax5</i>	0.32 ± 0.12	0.48 ± 0.32	0.38 ± 0.11	n.d.	0.65 ± 0.57	0.65 ± 0.18
<i>Pdk4</i>	1.44 ± 0.35	1.55 ± 0.53	1.15 ± 0.21	1.43 ± 0.07	3.28 ± 1.32	2.82 ± 0.10
<i>Prkdc</i>	0.63 ± 0.31	1.04 ± 0.04	0.62 ± 0.04	0.63 ± 0.08	0.77 ± 0.17	0.78 ± 0.03
<i>Ptch1</i>	0.42 ± 0.12	0.52 ± 0.07	0.32 ± 0.04	0.33 ± 0.08	0.61 ± 0.10	0.55 ± 0.03
<i>Rad51</i>	1.50 ± 0.46	1.98 ± 0.39	1.61 ± 0.18	1.48 ± 0.31	0.99 ± 0.19	0.87 ± 0.03
<i>Rpa1</i>	0.78 ± 0.27	1.04 ± 0.04	0.86 ± 0.01	0.83 ± 0.02*	0.69 ± 0.09	0.68 ± 0.08
<i>Runx1</i>	0.56 ± 0.22	0.74 ± 0.13	0.29 ± 0.07	0.37 ± 0.12	0.48 ± 0.13	0.51 ± 0.12
<i>Sfpi1</i>	0.89 ± 0.32	0.98 ± 0.13	3.04 ± 0.28	2.66 ± 0.06	1.25 ± 0.29	1.45 ± 0.05
<i>Slamf1</i>	0.23 ± 0.03	0.33 ± 0.07	0.00 ± 0.00	0.01 ± 0.00	n.d.	0.00 ± 0.00
<i>Smad7</i>	0.42 ± 0.16	0.40 ± 0.19	0.28 ± 0.06	0.25 ± 0.08	0.64 ± 0.19	0.54 ± 0.06
<i>Xiap</i>	0.45 ± 0.04	0.58 ± 0.12	0.50 ± 0.10	0.46 ± 0.08	0.48 ± 0.06	0.42 ± 0.04
<i>Xrcc5</i>	0.53 ± 0.09	0.63 ± 0.05	0.34 ± 0.06	0.34 ± 0.06	0.68 ± 0.26	0.60 ± 0.28
<i>Xrcc6</i>	0.85 ± 0.11	0.86 ± 0.02	1.01 ± 0.20	0.91 ± 0.11	1.16 ± 0.30	1.18 ± 0.17
<i>Zfpml</i>	1.06 ± 0.14	1.19 ± 0.42	0.05 ± 0.01	0.09 ± 0.05	0.20 ± 0.03	0.16 ± 0.01

MPPs isolated from either Cnt or *Atg12<sup>ckO</sup>* mice (n = 3) were used for Fluidigm gene expression analyses (3 technical pools of 100 cells/mouse). Results are mean ± SD and are expressed as fold changes compared to levels in Cnt HSCs; n.d., not detected, \*p ≤ 0.05; \*\*p ≤ 0.01, \*\*\*p ≤ 0.001.

**Supplementary Table 4 | Functional annotation of autophagy-deficient HSC ERBBS results**

<b>Hypomethylated DMRs</b>		
Term	Count	FDR
Phosphoprotein	380	8.8E-18
Nucleus	222	1.3E-06
Armadillo repeat-containing domain	8	2.9E-05
Transcription regulation	103	1.5E-04
Transcription	105	2.1E-04
Protein binding	205	2.6E-04
Alternative splicing	220	2.9E-04
Ubl conjugation	89	2.6E-03
Cadherin, N-terminal	13	7.0E-03
Membrane	310	8.6E-03
Nucleus	274	9.2E-03
Cytoplasm	296	1.2E-02
Cytoplasm	196	1.4E-02
Homophilic cell adhesion via plasma membrane adhesion molecules	20	2.0E-02
Transcription, DNA-templated	106	3.1E-02
Cell adhesion	34	5.2E-02
DNA-binding	84	8.2E-02
Receptor activity	19	9.0E-02
<b>Hypermethylated DMRs</b>		
Term	Count	FDR
Nucleus	56	1.5
Phosphoprotein	84	1.6

DAVID analyses of hypomethylated (FDR < .1) and hypermethylated (FDR < 2) differentially methylated regions (DMR) between Cnt and *Atg12<sup>ckO</sup>* HSCs (n = 4).

**Supplementary Table 5 | Functional annotation of activated HSCs ERBBS results**

Description	p-value	FDR
Spongiotrophoblast layer development	3.2E-08	1.0E-04
Cell differentiation involved in embryonic placenta development	7.2E-08	1.0E-04
Positive regulation of tyrosine phosphorylation of Stat3 protein	4.3E-07	5.0E-04
Negative regulation of transcription factor import into nucleus	7.0E-07	7.0E-04
Regulation of tyrosine phosphorylation of Stat3 protein	1.0E-06	8.0E-04
Tyrosine phosphorylation of Stat3 protein	2.3E-06	1.4E-03
Regulation of gliogenesis	3.9E-06	2.1E-03
Regulation of astrocyte differentiation	8.8E-06	4.1E-03
Gliogenesis	1.5E-05	6.1E-03
Positive regulation of tyrosine phosphorylation of STAT protein	1.7E-05	6.4E-03
Negative regulation of protein import into nucleus	2.3E-05	7.9E-03
Microtubule binding	1.1E-05	8.8E-03
Negative regulation of gliogenesis	3.2E-05	9.8E-03
Negative regulation of phosphorus metabolic process	4.0E-05	1.1E-02
Negative regulation of nucleocytoplasmic transport	4.0E-05	1.1E-02
Regulation of tyrosine phosphorylation of STAT protein	4.3E-05	1.1E-02
Visual learning	5.0E-05	1.2E-02
Negative regulation of transmembrane transport	7.0E-05	1.3E-02
Visual behavior	7.0E-05	1.3E-02
Negative regulation of intracellular protein kinase cascade	7.3E-05	1.3E-02
Regulation of transcription factor import into nucleus	7.4E-05	1.3E-02
Tyrosine phosphorylation of STAT protein	7.4E-05	1.3E-02
Negative regulation of intracellular protein transport	8.1E-05	1.3E-02
Positive regulation of JAK-STAT cascade	8.2E-05	1.3E-02
Myelin sheath	5.8E-05	1.4E-02
Basement membrane	6.6E-05	1.4E-02
Xenobiotic catabolic process	9.7E-05	1.5E-02
Transcription factor import into nucleus	1.1E-04	1.7E-02
Negative regulation of intracellular transport	1.3E-04	1.8E-02
Astrocyte differentiation	1.3E-04	1.8E-02

GO pathway analyses by ChIP-enrich of both hypomethylated and hypermethylated DMRs between qHSCs and aHSCs (FDR < 0.02) (n = 5).